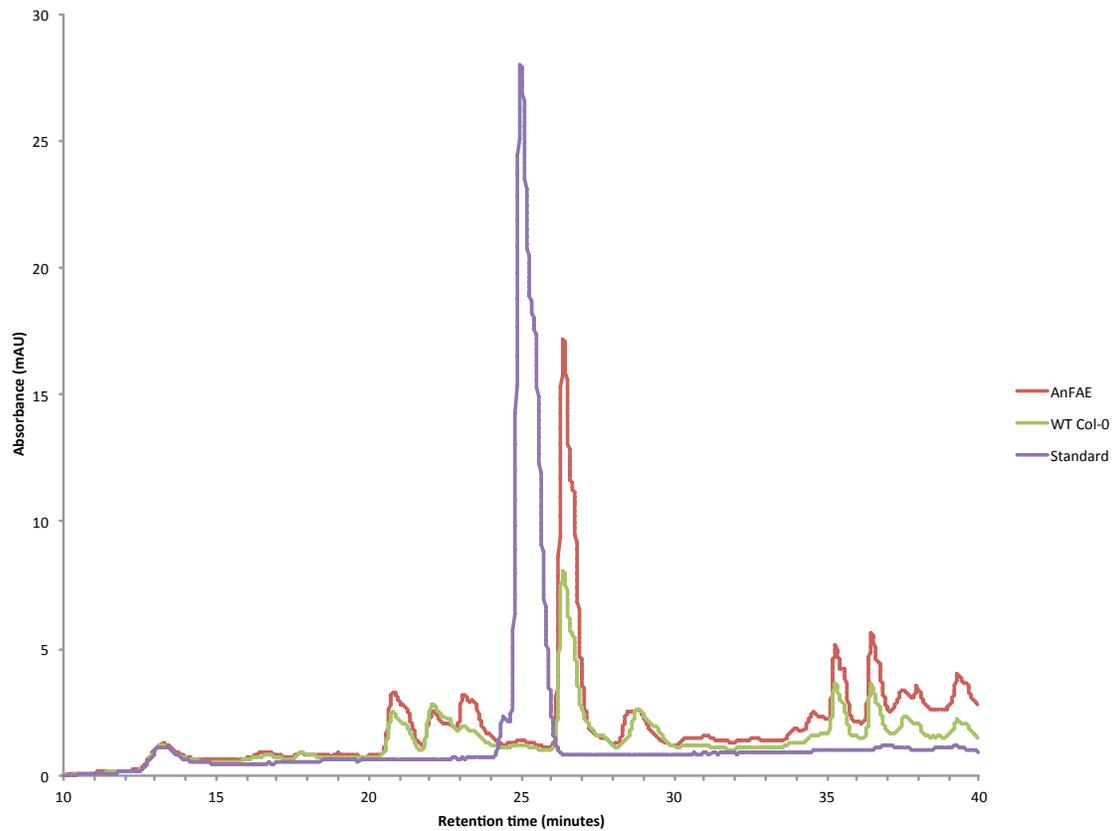
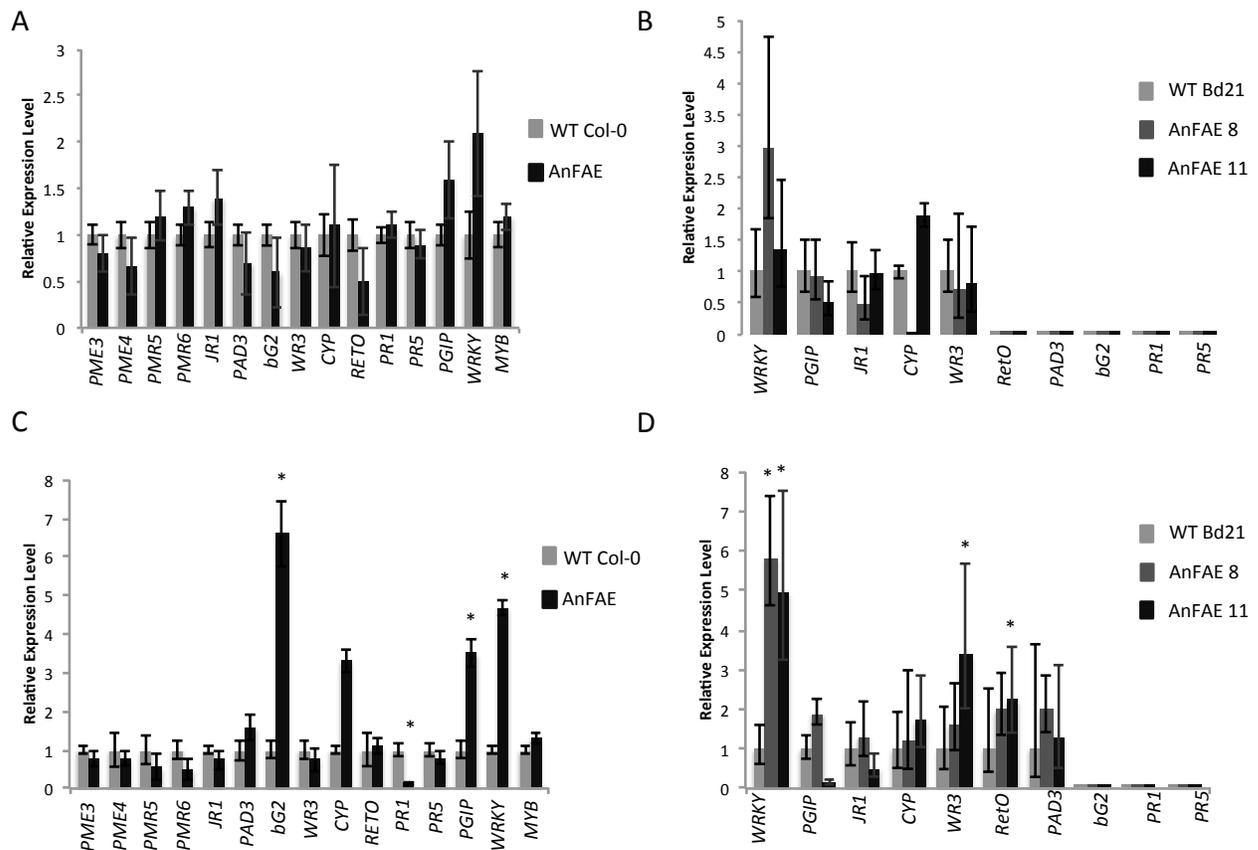


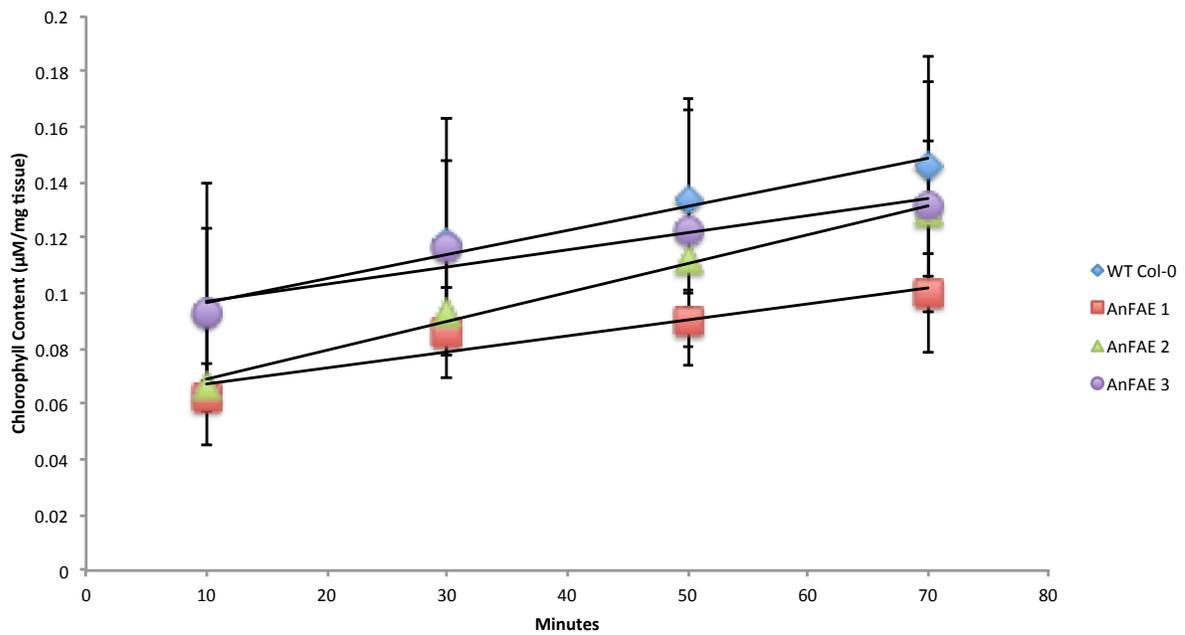
Supplementary Figure S1. Schematic diagram of expression cassettes used to express the genes in Arabidopsis (A) and Brachypodium (B) plants. Each cassette contains AnFAE from *Aspergillus nidulans* (AN5267.2) fused at the 3' end to smGFP (GFP), followed by a nopaline synthase (NOS) transcription terminator. Constructs used for transformation of Arabidopsis (A) contained four sequential CaMV 35S promoter regions for plant overexpression. To export this protein to the apoplast, a  $\beta$ -expansin signal peptide was fused to the 5' end of AnFAE. Constructs for Brachypodium transformation (B) contained the *Zea mays* ubiquitin gene promoter and its downstream intron (known to be required for suitable transcription). *Zea mays* ubiquitin signal peptide fused to the 5' end of AnFAE was used for export of protein to the apoplast.



Supplementary Figure S2. Analysis of the apoplast fluids from *AnFAE* (red) and wild-type Col-0 (green) plants using reverse-phase HPLC on a Prevail C18 5 $\mu$  column (4.6 x 250 mm; Grace Davison Discovery Sciences, Deerfield, IL, USA) with UV detection at 290 and 320 nm. Comparison of all obtained peaks with the chromatogram of the standard ferulic acid (purple) confirmed that plant apoplasts do not contain free ferulic acid.



Supplementary Figure S3. Real-time qPCR analysis for all genes used in this study. Pathogen-inducible defense genes in mock-treated plants (A-Arabidopsis, B-Brachypodium) and in infected plants 48 HPI (C-Arabidopsis, D-Brachypodium). Transcript levels in transgenic plants normalized to the expression of the same gene detected in wild-type plants (for which gene expression was set to 1), *ACTIN2* was used as the reference gene for Arabidopsis and *GAPDH* was used for Brachypodium. The comparative threshold cycle method was used for determining differences between transcript copy numbers in wild-type and transgenic plants. Data represent average obtained for three independent transgenic lines. Asterisks indicate significant differences between transgenic plants and wild-type plants (Student's *t*-test,  $P < 0.05$ ;  $n = 3$ ).



Supplementary Figure S4: Time-course of chlorophyll leaching from Arabidopsis leaves measurement using dimethyl sulfoxide with 10 minutes intervals. AnFAE 1, 2, and 3 represent three independent Arabidopsis lines expressing AnFAE. Error bars represent standard deviation. Samples were analyzed with student's t-test and no samples were found to be significantly different from WT Col-0.



Supplementary Figure S5. Peroxide accumulation in Arabidopsis and Brachypodium leaves by 3,3'-diaminobenzidine (DAB) incubation for 24 hours. Arabidopsis AnFAE 1, 2, and 3 represent three independent Arabidopsis lines expressing AnFAE, compared to wild type Col-0. Two Brachypodium lines, AnFAE 8 and AnFAE 11, were compared to wild type Bd21. Scale bars = 1 cm.

Supplementary Table S1. Primer sequences used in this work (5'-3'):

AtPR1-F: TCTAAGGGTTCACAACCAGG  
AtPR1-R: CCTTCTCGCTAACCCACATG  
AtPR5-F: GAGGATCGGGAGATTGCAAA  
AtPR5-R: GTCAGGGCAAGCGTTCCTGA  
AtbG2-F: GACGCAAATCTCGACTCGGT  
AtbG2-R: TCTCTATAGCTTCCCTGGC  
AtPAD3-F: ACTCTGGGAAAACGCAGATG  
AtPAD3-R: CTTTGGCTTCCTCCTGCTTC  
AtJR1-F: GTGTGCGGGCTACTATGACAA  
AtJR1-R: GGGCGCAACATTGACTCCAA  
AtWR3-F: TTCGTGCCTACGCGTTGAT  
AtWR3-R: CTATCTTGGCCTTCCTCTTC  
AtPGIP-F: CAGCTCAAGAATCTCGAGTT  
AtPGIP-R: TCGATCCGGTTAAAGTCGAT  
AtWRKY-F: CTAGAGACAATCCATCTCCA  
AtWRKY-R: TGCTGCAACGGGTGTTGAAG  
AtCYP-F: CAGCTGCACCACTTCTTGTT  
AtCYP-R: CACCAGGACACGTTCTTCGT  
AtRetO-F: AATGATGGATCGGATTCCGT  
AtRetO-R: ACCGCTTGGATTGCTTCCAA  
AtActin2\_F: GAAACCCTCGTAGATTGGCA  
AtActin2\_R: CTCTCCCGCTATGTATGTCCG  
AtPME3\_F: TTCAGGTGTGAAAGCTGACG  
AtPME3\_R: GTCCGACCATCTCCATAAAA  
AtPMR4\_F: TGATCGCACAGACTCAAAGG  
AtPMR4\_R: ATGATGCGAAGTCCTCTGCT  
AtPMR5\_F: GGCATCATCGTCTTCAGGAT  
AtPMR5\_R: CTGACGGATGACCGTCTTTT  
AtPMR6\_F: ACAAGGGCTTGTTCAGAGGA  
AtPMR6\_R: ATTCACCATCGTCCTTCGAG  
AtMyb46\_F: GCGCTTTCTCTCCTCAAGAA  
AtMyb46\_R: TGGGTGATGAGGATGAGTTG  
*B. cinerea* -Actin-F: AAGTGTGATGTTGATGTCC  
*B. cinerea* -Actin-R: CTGTTGGAAAGTAGACAAAG  
*B. cinerea* -PG1-F: TCTTTTACGCCCCTCCTTG  
*B. cinerea* -PG1-R: GATATCGCTGGAGGAACCAA  
*B. cinerea* -PG2-F: GTGGGATGGACTTGGCTCTA  
*B. cinerea* -PG2-R: ACCAGCATCTCCAGCAGAGT  
*B. cinerea* -PME3-F: TATCTCTGCCACACCACAA  
*B. cinerea* -PME3-R: ATGGTGCGGATATCGTTGTT  
BdPR1-F: ACGGTACGACTACTGGAGCAA  
BdPR1-R: GCCGCATGCCGACGTAGTTA

BdPR5-F: ACGGCGTACTCGAAGCTGTT  
BdPR5-R: CTAAGTAAACACGGTGCCTC  
BdbG2-F: GTTCAACGAGAACCAGAAGC  
BdbG2-R: AACAGACGATCGATCGATCG  
BdPAD3-F: AAGATATCCGGGCACGACGT  
BdPAD3-R: AGTCGAAGCTGCACAGTAGG  
BdJR1-F: CGGTCCATCACGTTTGTGAG  
BdJR1-R: CAGAAGAGGTAAGTTGGAGAG  
BdWR3-F: CCTTCTTCTTCTTCATCGAG  
BdWR3-R: CCGAGTATGCCTTGCAATAG  
AtActin2\_F: GAAACCCTCGTAGATTGGCA  
AtActin2\_R: CTCTCCCGCTATGTATGTCCG  
BdGAPD-F: GCTGGTGCCGATTATGTCGT  
BdGAPD-R: AGTGGTGCAGCTAGCATTTGAGACAAT  
BdRETO-F: CTAAGATCTTCGCCTGGCTA  
BdRETO-R: GCTGACGTACGGTTCATGA  
BdCYP-F: TTGATGCTGCCGTTCCGGAT  
BdCYP-R: TTCTGAAGCACGTCACGCAT  
BdWRKY-F: CTAATTAATCCCCATGCTCC  
BdWRKY-R: TGATCGTCAATCGACCCACT  
BdPGIP-F: TCTGGATGTCCCACAACAAC  
BdPGIP-R: TTGTGGCTCACGTCGAGGAA  
B. cinerea -Actin-F: AAGTGTGATGTTGATGTCC  
B. cinerea -Actin-R: CTGTTGGAAAGTAGACAAAG  
B. sorokiniana-GDP-F: ATCGAGCCCCACTACGCTGTA  
B. sorokiniana -GDP-R: TGACGGTCAGGTTGTTGCCGT